



# *Forensic Analysis using SNP and VNTR Signatures*

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# *Biothreat Agents*

- *B. anthracis*
- *Y. pestis*
  
- *Francisella tularensis*
- *Burkholderia mallei, pseudomallei*
- *Brucella melitensis, abortus, etc.*
  
- *E. coli* O157:H7
- *Salmonella*



# Molecular Microbial Forensics

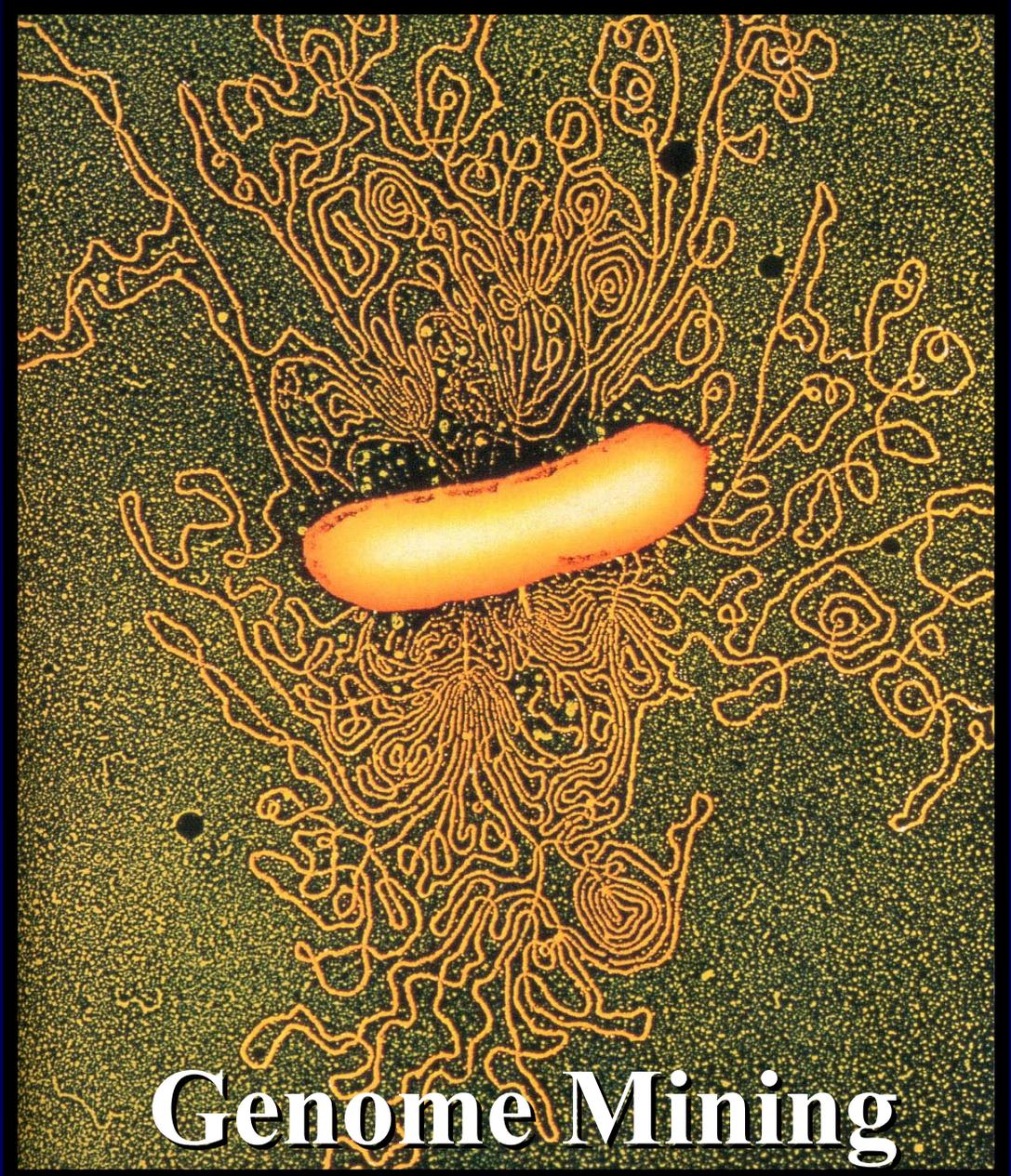
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- Molecular Assays
- Reference Databases
  - Population studies
- Real-life Validation Studies
- Models and Theory

*A genome is a  
complex and  
interesting  
place to work.*

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**Not all loci are  
created equal  
for diagnostics.**



**Genome Mining**

# High Resolution "DNA Fingerprinting"

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- Multiple-Locus VNTR Analysis (MLVA)
  - High Discrimination markers - rapidly mutating.
- Single Nucleotide Polymorphisms (SNPs)
  - Low Discrimination markers, but very stable!



# Evolutionary Scale and Mutation Rate

Fast

Slow

## Mutation Rate

$10^{-3}$

$10^{-4}$

$10^{-5}$

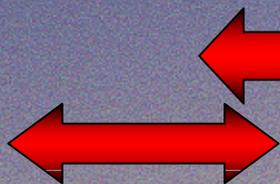
$10^{-6}$

$10^{-7}$

$10^{-8}$

$10^{-9}$

$10^{-10}$



SNR  
VNTRs



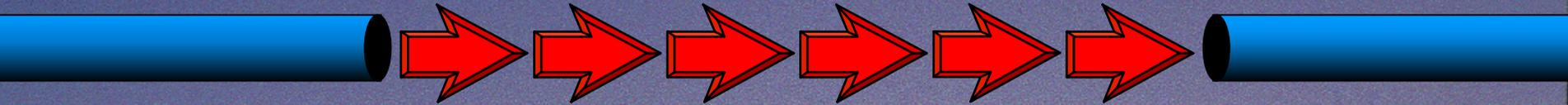
Complex VNTRs



SNPs



# Tandemly Repeated Sequences

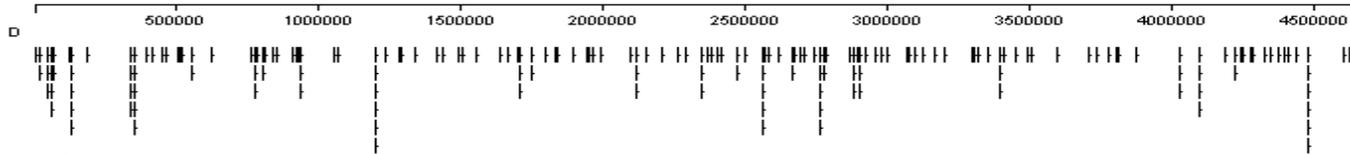


Genomic regions that vary greatly  
among worldwide isolates.

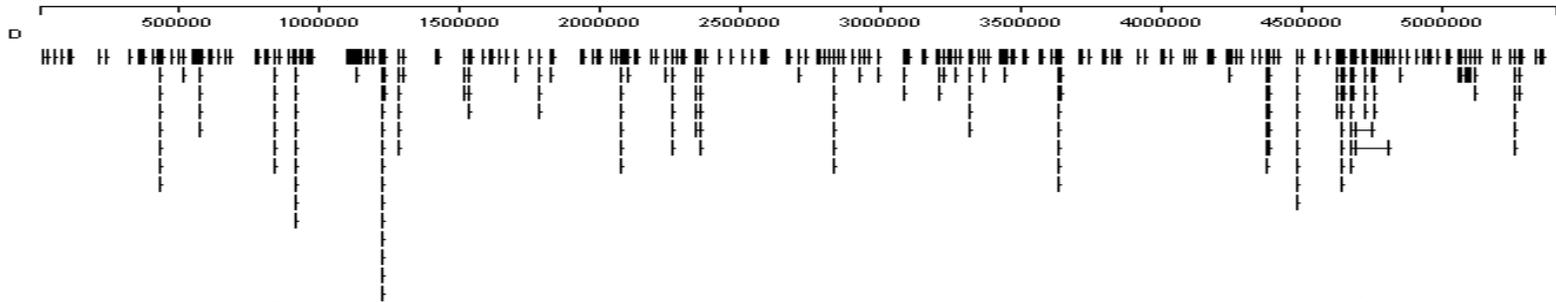
**VNTR**

# Genomic Tandem Arrays

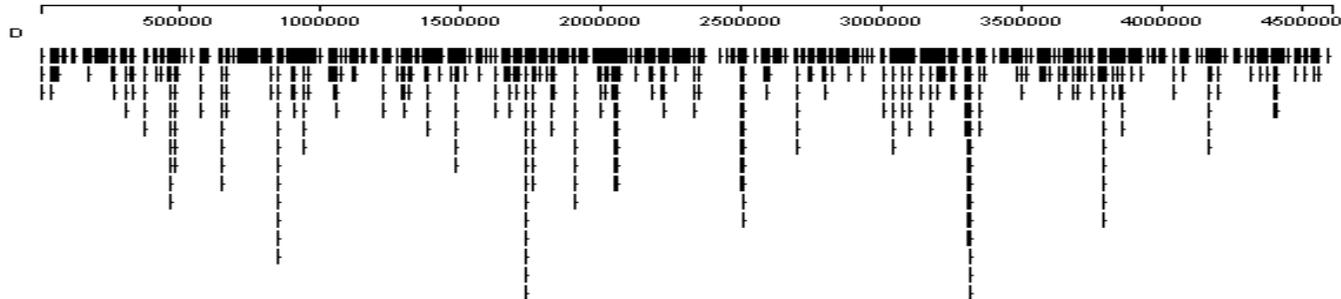
*E. coli* K12



*B. anthracis* Ames

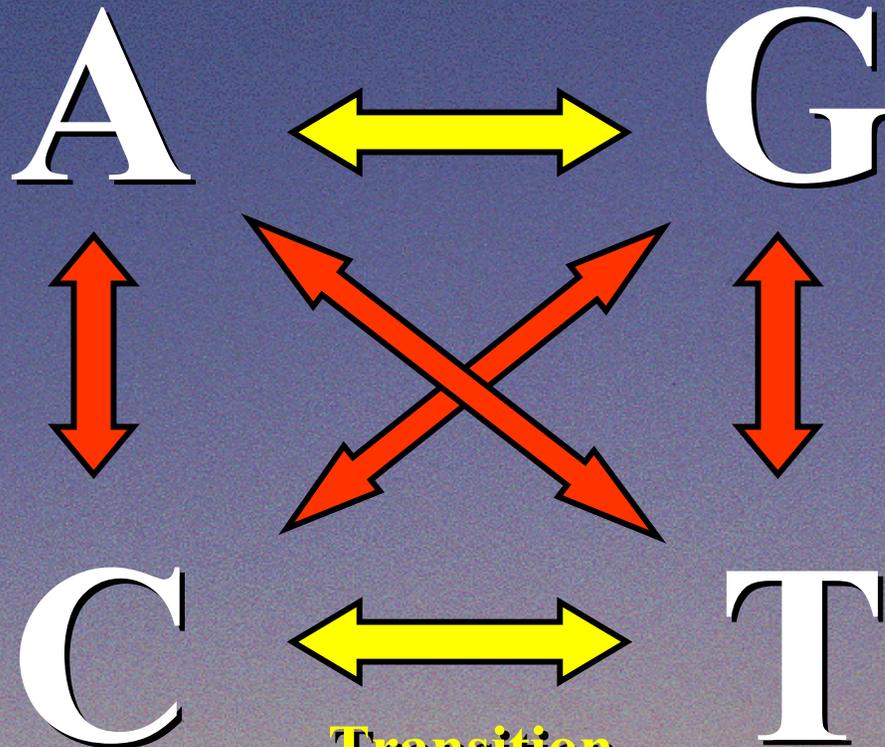


*Y. pestis* CO92



# DNA Sequence Evolution

Kimura 2-parameter model



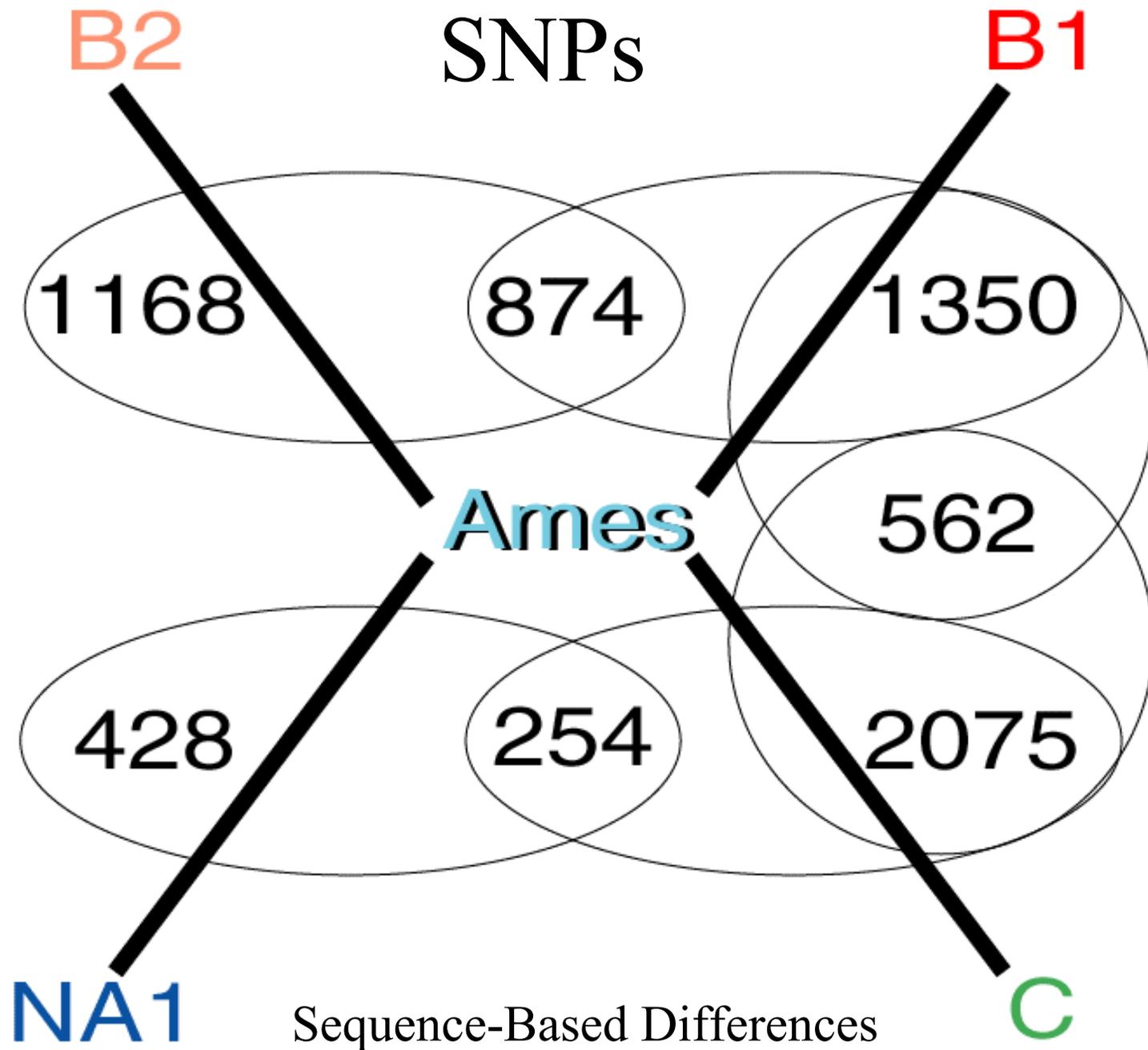
**Transversion  
Mutations**

**Transition  
Mutations**

# Two Approaches to SNP Discovery:

- **Limited Discovery:**
  - Multiple-Locus Sequence Typing  
*Appropriate when diversity is high.*
- **Exhaustive Discovery:**
  - Whole Genome Sequencing  
*Appropriate when diversity is low.*

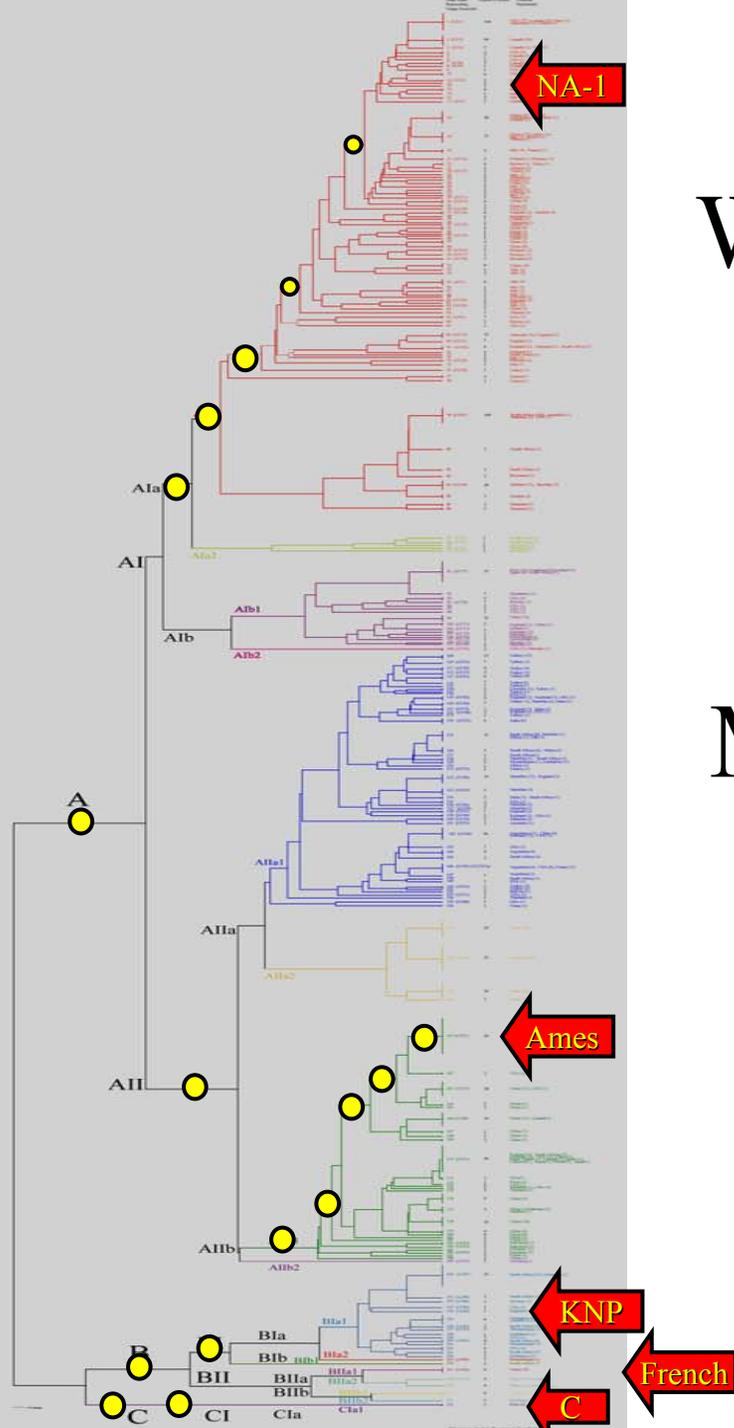




# Canonical Characters

- A phylogenetic character (such as a SNP) that defines an evolutionary point.
- In practice, SNPs are chosen to represent a whole groups of SNPs that mark a common phylogenetic branch.



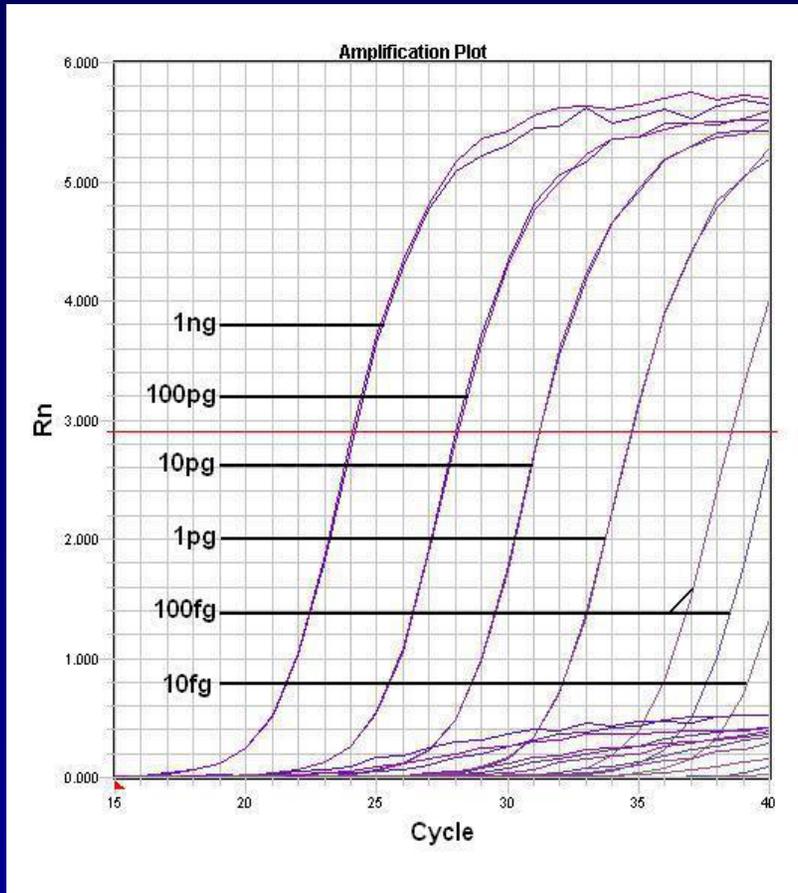


# World Wide *B. anthracis* Canonical SNPs

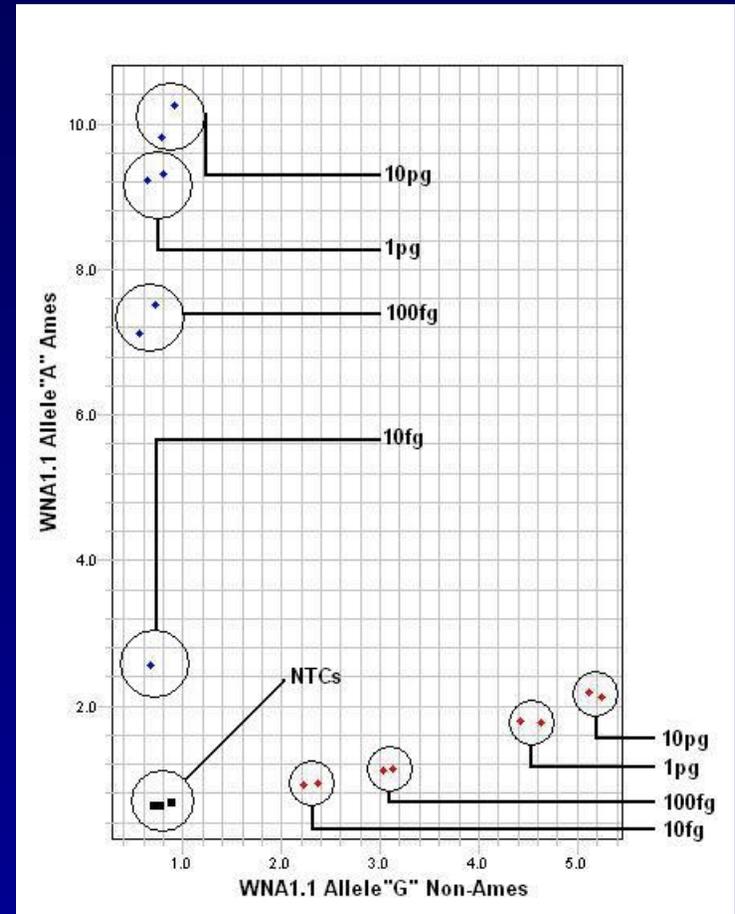
Marking major branches  
and specific strains

# Ames-Specific RT-PCR

a)

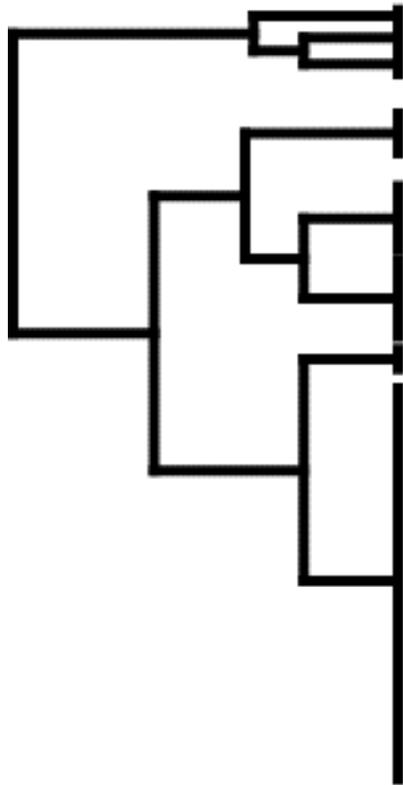


b)



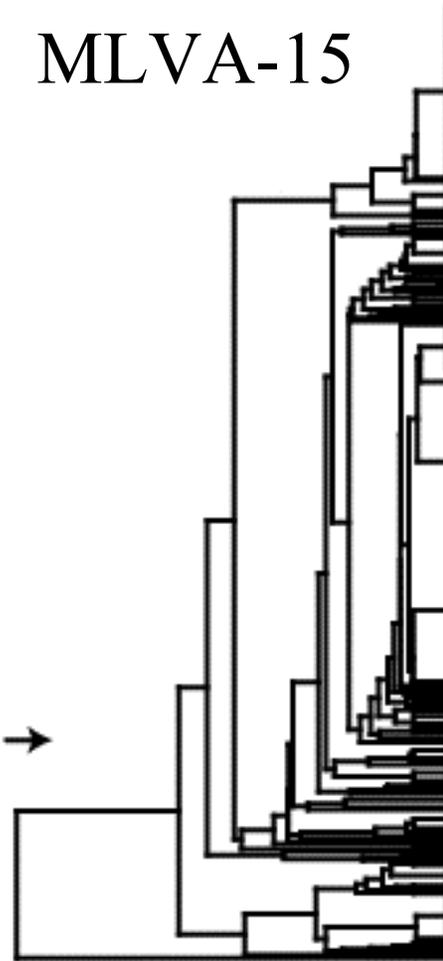
# *B. anthracis* PHRANA (1067 isolates)

Canonical SNPs



8 subtypes

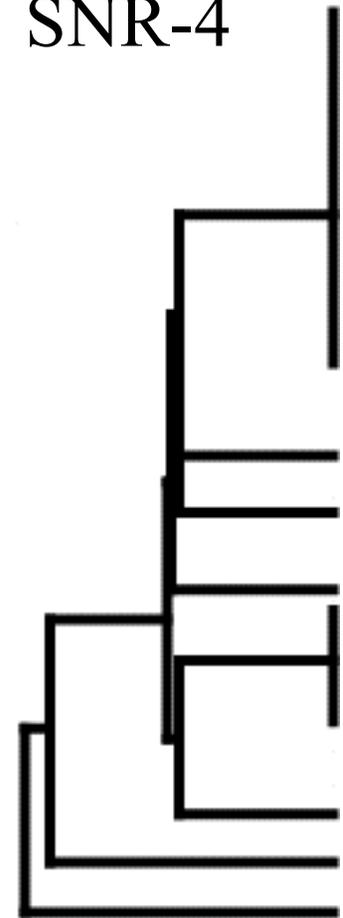
MLVA-15



108 subtypes

(208 GTs)

SNR-4



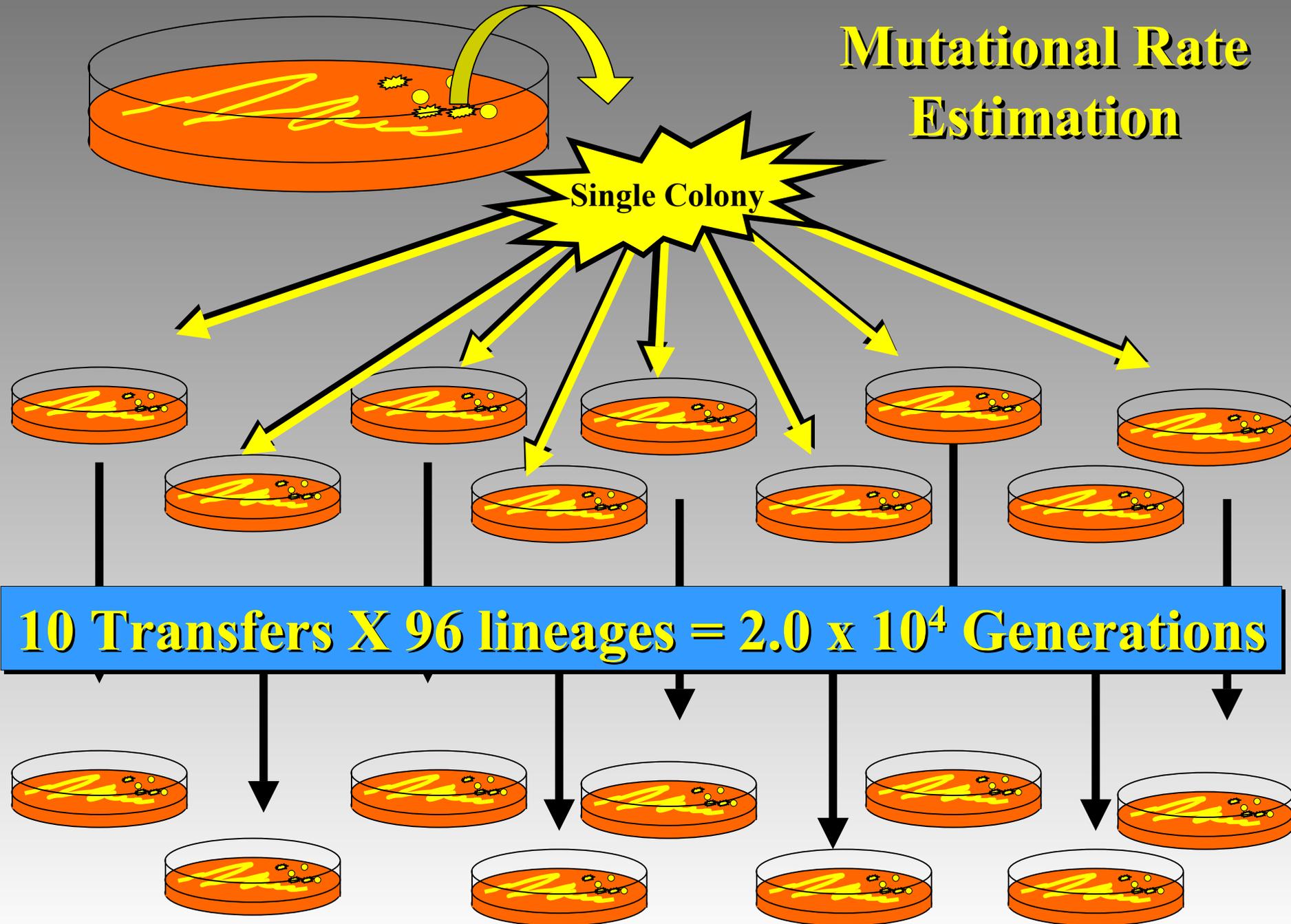
8 subtypes

(476 GTs)

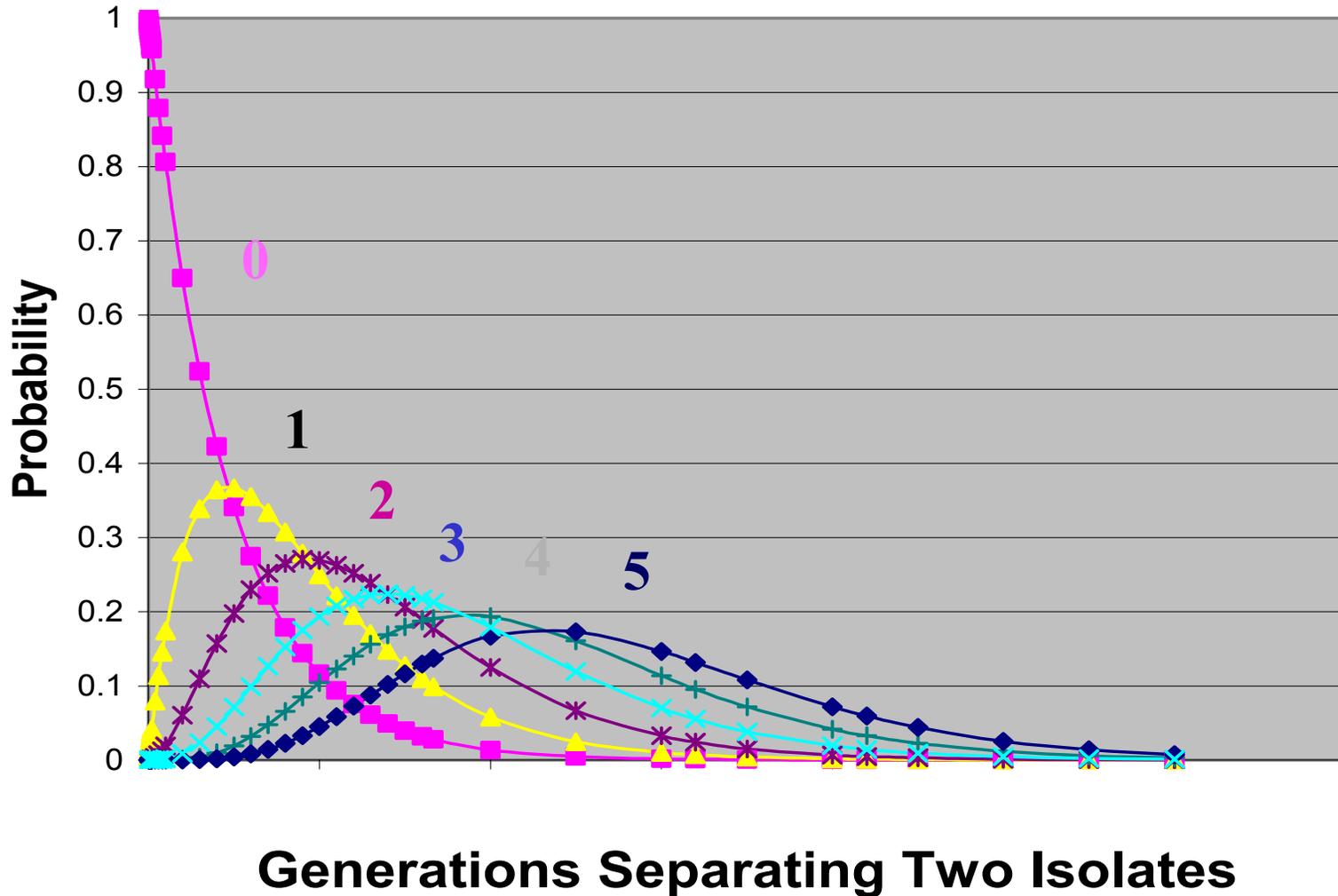
600  
Isolates →

57  
Isolates →

# Mutational Rate Estimation



# Mutation Rate Models



# Anthrax Letter Attacks

4TH GRADE  
GREENDALE SCHOOL  
FRANKLIN PARK NJ 08852



SENATOR LEAHY  
433 RUSSELL SENATE OFFICE  
BUILDING  
WASHINGTON D.C. 20510-4502

20520+4502



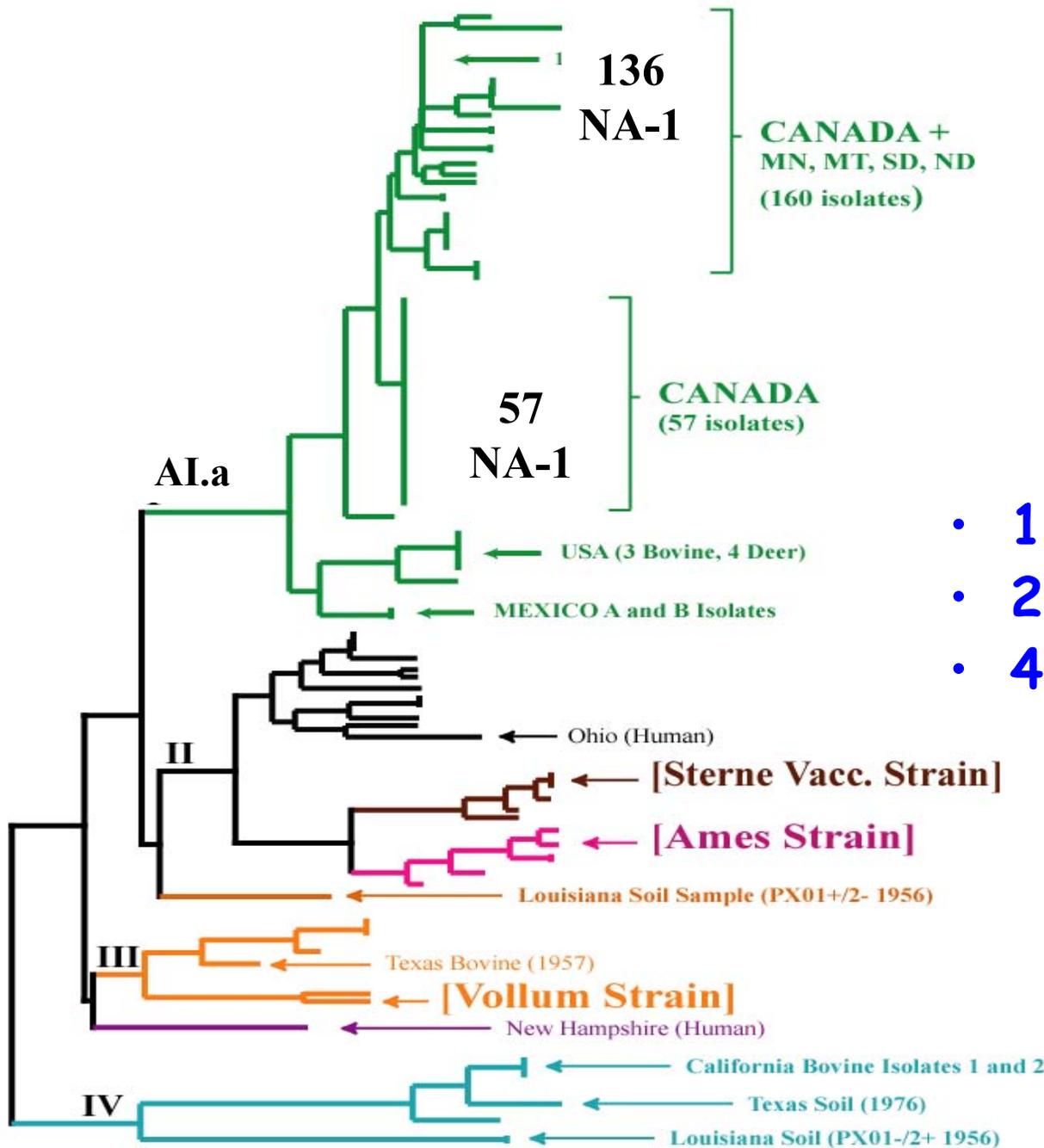


4363

BRRAT0025  
BT000676-01  
4 OCT 2001

BACTERIA

# North America Anthrax



- 15 VNTR Analysis
- 269 Isolates
- 47 genotypes

*Matt Van Ert  
unpublished*

# Molecular Forensics Analysis

## Testimony in Court

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- "A match - Inclusion"
  - Failure to exclude, could be the source.
- "Exclusion"
  - Very different and unlikely the same.
- "Kind of Close?"
  - Maybe yes? Maybe no?

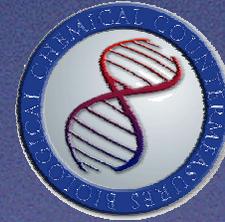
# Collaborators

- TIGR
  - Jacques Ravell, Tim Read
- CDC Atlanta
  - Alex Hoffmaster, Tanja Popovic
- CDC Ft. Collins
  - May Chu, Ken Gage, Jennifer Lowell
- Louisiana State University
  - Martin Hugh-Jones, Pamala Coker
- Institut Pasteur
  - Agnes Fouet, Michele Mock, Elisabeth Carniel
- Umeå Sweden Group
  - Anders Johansson, Mats Forsman, Anders Sjöstedt
- Livermore National Lab
  - Gary Andersen, Emilio Garcia, Patrick Chain, Peter Agron
- Los Alamos
  - Paul Jackson, Rich Okinaka, Karen Hill
- Keim Lab Characters
  - Talima Pearson, Joseph Busch,
  - Tatum Simonson, Shane Rhoton
  - Jana U'Ren, Ryan Easterday,
  - Matt Van Ert, Meghan Dukerich,
  - Lynn Huynh, Shaylan Zanecki,
  - Zack Jay, Michelle Maldonado,
  - Amy Vogler, Jessica Girard,
  - Kimothy Smith, Leo Kenefic,
  - Ryan Easterday, Chris Allender
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**Bio-Chem Countermeasures**



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**Pathogen Evolution -NIGMS**